MULTIMEDIA UNIVERSITY*

STUDENT ID NO

MULTIMEDIA UNIVERSITY

FINAL EXAMINATION

TRIMESTER 1, 2015/2016

HPB2031 – Bioinformatics Algorithms I

(All sections / Groups)

05-Oct-2015
09:00 a.m-11 a.m
(2 Hours)

INSTRUCTIONS TO STUDENTS

1. This question paper consists of 3 pages, including this cover page.
2. You are required to attempt four (4) questions out of five (5) questions. All questions carry equal marks (10).
3. Please write all your answers in the Answer Booklet provided.

Question 1

a) Explain DOT matrix method in sequence alignment? What are the parameters uses for filtering technique in DOT matrix?

[4 marks]

b) Construct the Global alignment scoring matrix for given TWO sequences as below:
Seq 1 = AAGCCT
Seq 2 = GCCTT

Match = +2, Mismatch= -1, Gap= -2

Perform the trace-back steps in order to get an optimal alignment.

[4 marks]

c) Briefly explain any TWO differences between PAM and BLOSUM substitution matrices?

[2 marks]

Question 2

a) Briefly explain the differences between sequence similarity and sequence homology?

[2 marks]

b) Briefly explain Biological databases. What are the differences between Primary and Derivative databases?

[5 marks]

c) Briefly explain the different types of methods used in multiple sequence alignment with example?

[3 marks]

Question 3

a) What are the variants of BLAST program? Explain about the database connected to the BLAST program?

[4 marks]

b) Briefly discuss the Steps involve in BLAST algorithm?

[4 marks]

c) What are the similarities of the logic of BLAST and FASTA methods in sequence analysis?

[2 marks]

Continue…

Question 4

a) Given the following distance matrix, construct the corresponding phylogenetic tree using the distance method (UPGMA). [7 marks]

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

b) What is a phylogenetic profile? [1 mark]
What inferences about the proteins can you make from the profile given below? [2 marks]

Protein	Genome		
	G1	G2	G3
P1	0	1	1
P2	0	0	1
P3	1	0	0
P4	0	1	1

Question 5

a) What are metabolic pathways and how do they contribute to the functions of life? [3 marks]

b) List three (3) differences between the KEGG and BioCyc pathway databases? [3 marks]

c) Pathway modeling software such as VANTED can find "links" between chemicals in a pathway. What do these links tell you about those chemicals? [2 marks]

d) What are the components and features of a pathway which you must know in order to model the pathway? [2 marks]

END OF PAPER